

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 26, 2004, 08:40:32 ; Search time 16 Seconds  
(without alignments) 2.323 Million cell updates/sec

Title: us-09-989-730-401

Perfect score: 993

Sequence: 1 MPVPALCLLWALAMVTRPAS.....AQOHLRQIQERLHTAALPA 198

Scoring table:	BLOSUM62	
Xgapop	10.0	Xgapext 0.5
Ygapop	10.0	Ygapext 0.5
Fgapop	6.0	Fgapext 7.0
Delop	6.0	Delext 7.0

Searched: 45 seqs. 93847 residues

Total number of hits satisfying chosen parameters: 90

Minimum DB seq length: 0

Maximum DB size: 2000000000  
Maximum DB size length: 2000000000

Post-processing: Minimum Match: 0%

100% Processing: Minimum Match 0% Maximum Match 100%

Maximum Match 100%  
Listing first 45 summaries

Command Line parameters:

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-Model=frame+beta.model -DRV=soft -Q=us-09-989-730-401 -DB=tni401.seq
-SUFFIX=ptc -START=us-09-989-730-401.tni -MINMATCH=0.1 -LOOP=0.0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=tblsum62 -TRANS=human0.cdd -LIST=45
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-COUTPUT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO XILPY -NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOF=10 -XGAPEXT=0.5 -FGAPOF=6
-FGAPEXT=7 -YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELOEXT=7

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Database : rni401.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

 $\partial$ 

Result No.	Score	Query Match	DB Length	ID	Description
1	897.5	90.4	990	1	US-09-369-247-16 Sequence 16. April

```

, RESULT 1
, US-09-369-247-16
, Sequence 16, Application US/09369247
, Patent No. 6569992
, GENERAL INFORMATION:
, APPLICANT: Rosen et al.
, TITLE OF INVENTION: 44 Human Secreted Proteins
, FILE REFERENCE: P2024p1
, CURRENT APPLICATION NUMBER: US/09/369,247
, CURRENT FILING DATE: 1999-08-05
, EARLIER APPLICATION NUMBER: 60/074,118
, EARLIER FILING DATE: 1998-02-09
, EARLIER APPLICATION NUMBER: 60/074,157
, EARLIER FILING DATE: 1998-02-09
, EARLIER APPLICATION NUMBER: 60/074,137
, EARLIER FILING DATE: 1998-02-09
, EARLIER APPLICATION NUMBER: 60/074,341
, EARLIER FILING DATE: 1998-02-09
, EARLIER APPLICATION NUMBER: 60/074,141
, EARLIER FILING DATE: 1998-02-09
, NUMBER OF SEQ ID NOS: 172
, SOFTWARE: PatentIn ver. 2.0
, SEQ ID NO 16
, LENGTH: 990
, TYPE: DNA
, ORGANISM: Homo sapiens
, US-09-369-247-16

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Alignment Scores:	
Pred. No.:	0
Score:	897.50
Percent Similarity:	82.55%
Best Local Similarity:	82.13%
Query Match:	90.38%
DG:	1
Gaps:	1
Indels:	39
Mismatches:	4
Conservative:	1
Matches:	193
Length:	990

us-09-989-730-401 (1-198) X US-09-369-247-16 (1-990)

1 MetProValProAlaLeuCysLeuLeuTrpAlaLeuAlaMetValThrArgProAlaSer 20  
3 ATGCCAGTCCCTACTCTGTGCGCTGTGGGGCCCTGGCAATGTCACCGGCGCTGCTCA 62

21 A A A A P r o M e t G l y P r o G l u L e u A l a G i n H i s G l u G l u L e u T h r L e u L e u P h e H i s 40  
63 G C G S C C C C A T G S C G S C C C A G A C T G C A C A G C A T G A G S A G T G A C C T G C T T C C A C 120  
d b

# Appendix A

us-09-989-730-401.rni

Qy	41	GlyThrLeuGlnLeuGlyGlnAlaLeuAenGlyValTyrArgThrThrCluGlyArgLeu	60
Db	123	GGGACCTTGCGCTGGGCCAGGCCCTCAACGGGTGTACAGGACCACCGAGCGGCTG	182
Qy	61	ThrLysAlaArgAsnSerLeuGlyLeuTyrGlyArgThrIleGluLeuGlyGlnGlu	80
Db	183	ACAAAGGCCAGGACAGCTGGGTCTCTATGGCGGCACATAGAACTCTCTGGGCGAGAG	242
Qy	81	ValSerArgGlyArgAspAlaAlaGlnGluLeuArgAlaSerLeuLeuGluThrGlnMet	100
Db	243	GTACGCCGGGGCGGGATGCGCCAGGAACCTTCGGGCAAGCCTGTTGGAGACTCAGATG	302
Qy	101	GluGluAspIleLeuGlnLeuGlnAlaGluAlaThrAlaGluValLeuGlyGlnValala	120
Db	303	GAGCAGGATATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTCTCTGGGGAGGTGCC	362
Qy	121	GlnAlaGlnIleValLeuArgAspSerValGlnArgLeuGluValGlnLeuArgSerAla	140
Db	363	CAGGCACAGAGGTGCTACCGGACAGCGTKCAGCGCTAGAACTCCAGTTAGAGCGCC	422
Qy	141	TrpLeuGlyProAlaTyrArgGluPheGluValLeuLysAlaHisAlaAspLysGln--S	160
Db	423	TGGCTGGGGCTGCTACCGAGATTTGAGGTCTTAAAGGCTCAAGCTGACCAAGCAGAG	482
Qy	160	erHisIleLeuTrpAlaLeuThrGlyHisValGlnArgGlnArgGluMetValalaG	180
Db	483	CCCATCTCTATGACC-CTCAGAGGCCAGCT-CAGCGCAGAGCGGGAGATGTTGGCAC	540
Qy	180	GlnHisArgLeuArgGlnIleGlnGlu-----	189
Db	541	AGCAGCATCGGCTGCCACAGATCCAGGAGAGGTGAGCTGGCAGGGGTTGGCAGGCAGG	600
Qy	189	-----	189
Db	601	GCAGTTGGATGGGGGGGCACAGGCAGCTGGAAAGGGGCCCCCTCACCTGGGCTGAGCC	660
Qy	190	-----ArgLeuHisThrAlaAlaLeuProAla	198
Db	661	ACATCTCCCTCCCGAGACTCCACACAGCGGCGCTCCAGCC	701

Appendix A

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 26, 2004, 08:40:32 ; Search time 16 Seconds  
(without alignments)  
2.323 Million cell updates/sec

Title: us-09-989-730-401  
Perfect score: 993  
Sequence: 1 MEVPALCLLWALWTRPAS.....AQQHRLQIQERLHTAALPA 198

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 45 seqs, 93847 residues

Total number of hits satisfying chosen parameters: 90

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Command line parameters:  
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-SUFFIX=ptc -OUT=us-09-989-730-401.rni -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
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-FGAPEXT=7 -FGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : rni401.seq:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897.5	90.4	990	1	US-09-369-247-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-369-247-16  
; Sequence 16, Application US/09369247  
; Patent No. 6569992  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 44 Human Secreted Proteins  
; FILE REFERENCE: P2024P1  
; CURRENT APPLICATION NUMBER: US/09/369,247  
; CURRENT FILING DATE: 1999-08-05  
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; EARLIER APPLICATION NUMBER: 60/074,141  
; EARLIER FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-369-247-16

Alignment Scores:  
Pred. No.: 0  
Score: 897.50  
Percent Similarity: 82.55%  
Best Local Similarity: 82.13%  
Query Match: 90.38%  
DB: 1  
Length: 990  
Matches: 193  
Conservative: 1  
Mismatch: 4  
Indels: 39  
Gaps: 1

us-09-989-730-401 (1-198) x US-09-369-247-16 (1-990)

QY	1	MetProValProAlaLeuCysLeuLeuTtpAlaLeuAlaMetValThrArgProAlaSer	20
DB	3	ATGCCAGTGGCTACTCTGTGGCCCTGGCAATGGTGACCCGGGCTGCTCA	62
QY	21	AlaAlaProMetGlyGlyProGluLeuAlaGlnHisGluLeuThrLeuLeuPheHis	40
DB	63	CGGGCCCCCATGGSCGGCCAGAACTGGCACAGCATGAGAGCTGACCTGTCTTCCAC	121

Appendix A

us-09-989-730-401.rni

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QY 41 GlyThrLeuGlnLeuGlyGlnAlaLeuAsnGlyValTyrArgThrThrGluGlyArgLeu 60
Db 123 GGGACCTTCGACGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCCACGGAGGGAGCGGCTG 182
QY 61 ThrLysAlaArgAsnSerLeuGlyLeuTyrGlyArgThrIleGluLeuGlyGlnGlu 80
Db 193 ACNAGGCCAGGAACAGCCTGGGTCCTATGGCCGACATAGAACTCTGGGGCAGGAG 242
QY 81 ValSerArgGlyArgAspAlaAlaGlnGluLeuArgAlaSerLeuLeuGlnThrGlnMet 100
Db 243 GTCAGCCGGGGCCGGGATGCGAGCCAGCAACTTCGGGGCAAGCCTGTGTGGAGACTCAGATG 302
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Db 303 GAGGAGGATATTCGACGCTGCGGACAGAGGCCACACAGCTGAGGTGCTGGGGAGGTGGCC 362
QY 121 GlnAlaGlnLysValLeuArgAspSerValGlnArgLeuGluValGlnLeuArgSerAla 140
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QY 141 TrpLeuGlyProAlaTyrArgGluPheGluValLeuIleValAlaHisAlaAspLysGln--S 160
Db 423 TGGCTGGGCCCTGGCTACCGAGATTGAGGTCTTAAAGCTCACGCTGACCAAGCAAGAG 482
QY 160 ArgHisIleLeuTyrAlaLeuThrGlyHisValGlnArgGlnArgGluMetValAlaG 180
Db 483 CCCATCCTATGGCC-CTCACAGGCCACGT-CAGCGGCGAGAGCGGGAGATGGTGGCAC 540
QY 180 GlnHisArgLeuArgGlnIleGlnGlu----- 189
Db 541 AGCAGCATCGGCTGCGACAGATCCAGGAGAGGTGAGCTGGCAGGGGTTTGGCAGGCAGG 600
QY 189 ----- 189
Db 601 GCAGTTGGATGGGGGGCGCACAGGGCAGCTGGAAAGGGGGCCCTCCTCAGCTGGGGCTGAGCC 660
QY 190 -----ArgLeuHisThrAlaAlaLeuProAla 198
Db 661 ACATCTCCCTCCCGAGACTCCACACAGCGGCGCTCCCGACC 701
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 08:17:52 ; Search time 73 Seconds  
(without alignments) 4.114 Million cell updates/sec

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Title:          US-09-989-730-400
Perfect score:  893
Sequence:       1 gtcatgcagtcgcctctt.....aaaaaaaaaaaaaaaaaa 893
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Scoring table: IDENTITY\_NUC  
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Searched: 45 seqs, 168143 residues

Total number of hits satisfying chosen parameters: 90

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : rni400.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Best Local Similarity 86.9%; Pred. No. 3.6e-16;  
Matches 855; Conservative 8; Mismatches 13; Indels 108; Gaps 4;

3 CATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTC 62

2 CATGCCAGTGCCTACTCTGTGCCTGCTGTGGGCCCTGGCAATGGTGACCCGGCCTGCCTC 61

63 AGCGGCCCCCATGGGCGGCCAGAACTGGCA CAGCATGAGGAGCTGACCCCTGCTCTTCCA 122

62 AGCGGCCCCCATGGSSCGGGCCAGAA CTGGCA CAGCATGAGGAGCTGACCCCTGGCTCTTCCA 121

123 TGGGACCGTGCAGCTGGGGCCAGGCCCTCAACGGTGTGTACAGGACCAAGGAGGGGACGGCT 182

122 CCGGACCGTTCAGCTGGGCGAGGGCCCTCA CCGTCTCTACAGGACCTACGGATGGCA CCGCT 181

[illegible]

183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1

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## ALIGNMENTS

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1  RESULT 1
2  ; Sequence 16, Application US/09369247-16
3  ; Patent No. 6569992
4  ; GENERAL INFORMATION:
5  ; APPLICANT: Rosen et al.
6  ; TITLE OF INVENTION: 44 Human Secreted Proteins
7  ; FILE REFERENCE: P2024P1
8  ; CURRENT APPLICATION NUMBER: US/09/369,247
9  ; CURRENT FILING DATE: 1999-08-05
10 ; EARLIER APPLICATION NUMBER: 60/074,118
11 ; EARLIER FILING DATE: 1998-02-09
12 ; EARLIER APPLICATION NUMBER: 60/074,157
13 ; EARLIER FILING DATE: 1998-02-09
14 ; EARLIER APPLICATION NUMBER: 60/074,137
15 ; EARLIER FILING DATE: 1998-02-09
16 ; EARLIER APPLICATION NUMBER: 60/074,341
17 ; EARLIER FILING DATE: 1998-02-09
18 ; EARLIER APPLICATION NUMBER: 60/074,141
19 ; EARLIER FILING DATE: 1998-02-09
20 ; NUMBER OF SEQ ID NOS: 172
21 ; SOFTWARE: PatentIn Ver. 2.0
22 ; SEQ ID NO 16
23 ; LENGTH: 990
24 ; TYPE: DNA
25 ; ORGANISM: Homo sapiens
26 ; US-09-369-247-16

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us-09-989-730-400.rni

363	QY	CGAGCACAAGAGTGCTACGGGACAGCTGCAGCGGCTAGAACTCCAGCTCAGAGAGCCG	422
362	Db	CGAGCACAAGAGTGCTCAGGGA	421
423	QY	CTGGCTGGGCGCTCCCTACCGAGAAATTTGAGGTCTTTAAAGGGTCTCAGCTGACAAGC-AGA	481
422	Db	CTGGCTGGGCGCTCCCTACCGAGAAATTTGAGGTCTTTAAAGGGTCTCAGCTGACAAGCAAGA	481
482	QY	GCCACATCCTATGGGCGCTCACAGGCCACGCTGCAGCGGCAGAGGGGGGAGATGGTGGCAC	541
482	Db	GCCACATCCTATGGGCGCTCACAGGCCACGT-CAGCGGCAGAGCGCGGAGATGGTGGCAC	540
542	QY	AGCAGCATGGCTCGACAGATCCAGGAG	570
541	Db	AGCAGCATGGCTCGACAGATCCAGGAGAGGTGAGCTCGCAGCGGTTTGGCAGGCAGG	600
571	QY	GCAGTTGGATGGGGGGCGCACAGGGCAGCTGGAAGGGGGCCCCCTCACCTGGGCTGAGCC	570
601	Db	GCAGTTGGATGGGGGGCGCACAGGGCAGCTGGAAGGGGGCCCCCTCACCTGGGCTGAGCC	660
571	QY	AGACTCCACACAGCGGCGGTCCGACGCTGAATCTGCCTGGATGAA	616
661	Db	ACATCTCCCTCCCCAGACATCCACACAGCGCGCTCCGAGCTCTGAATCTGCCTGGATGAA	720
617	QY	CTGAGGACCAATCATGCTGCAAGAAACACTTCCACGCCCCGTGAGGCCCTCTGCAGAGGA	676
721	Db	CTGAGGACCAATCATGCTGCAAGAAACACTTCCACGCCCCGTGAGGCCCTCTGCAGAGGA	780
677	QY	GGAGTGGCTGTTCATCGGATCATGCGGGCGCGGGGCCCACTTCTGAGCAACAAGACA	736
781	Db	GGAGTGGCTGTTCATCGGGAATGACGAGCGCGCGGGGCCCACTTCTGAGCAACAAGACA	840
737	QY	GAGACAGACGCGGCGGGAACAAGGCAGAGATGTAG-CCCCATTGGGGAGGGGTGGAG	795
841	Db	GAGACAGACGCGGCGGGAACAAGGCAGAGATGTAGTCCCCATTGGGGAGGGGTGGAG	900
796	QY	GAAAGACATGTACCCCTTTCATGCCCTACACCCCTCATTAAGCGAGTCTGGCATTTTC	855
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961	Db	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	984

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 08:17:52 ; Search time 73 Seconds  
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Title: us-09-989-730-400  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 0.5

Searched: 45 seqs, 168143 residues

Total number of hits satisfying chosen parameters: 90

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : rni400.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	758	84.9	990	1	US-09-369-247-16

#### ALIGNMENTS

RESULT 1  
US-09-369-247-16  
; Sequence 16, Application US/09369247  
; Patent No. 6569992  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 44 Human Secreted Proteins  
; FILE REFERENCE: P2024P1  
; CURRENT APPLICATION NUMBER: US/09/369,247  
; CURRENT FILING DATE: 1999-08-05  
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; EARLIER APPLICATION NUMBER: 60/074,141  
; EARLIER FILING DATE: 1998-02-09  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-369-247-16

Query Match 84.9%; Score 758; DB 1; Length 990;  
Best Local Similarity 86.9%; Pred. No. 3.6e-16;  
Matches 855; Conservative 8; Mismatches 13; Indels 108; Gaps 4;

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Qy	63	AGCGGCCCCCATGGCGGCCAGAACTGGACAGCATGAGGAGCTACCTGCTCTTCCA	122
Db	62	AGCGGCCCCCATGGCGGCCAGAACTGGACAGCATGAGGAGCTACCTGCTCTTCCA	121
Qy	123	TGGGACCTTCAGCTGGCGCCAGCCCTCAACGGTGTGTACAGCACCGAGGAGCGGCT	182
Db	122	CGGACCCCTCAGCTGGCGCCAGCCCTCAACGGTGTGTACAGCACCGAGGAGCGGCT	181
Qy	183	GACAAAGGCCAGGAACAGCTGGTCTCTATGGCCCGCACATAGAACTCTTGGGCGAGGA	242
Db	182	GACAAAGGCCAGGAACAGCTGGTCTCTATGGCCCGCACATAGAACTCTTGGGCGAGGA	241
Qy	243	GGTACGCCGGGCGGGGATGACGCCAGGAACTTGGGCGAGGAGCTTTGGAGACTCAGAT	302
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Qy	303	GGAGGAGGATATTCTGCAGCTGCAGGCGCCACAGCTGAGGTCTGGGGAGGTGGC	362
Db	302	GGAGGAGGATATTCTGCAGCTGCAGGCGCCACAGCTGAGGTCTGGGGAGGTGGC	361

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363	QY	CGAGCACAAGAGTGCTACGGGACAGCTGCAGCGGTAGAGTCTCAGCTGCAGAGCGC	422
362	Db	CGAGCACAAGAGTGCTACGGGACAGCTGCAGCGGTAGAGTCTCAGCTGCAGAGCGC	421
423	QY	CTGGCTGGGGCCCTCCCTACCGAGAAATTTAGGTTCTTAAAGGCTCAGCTGCACAGC-AGA	481
422	Db	CTGGCTGGGGCCCTCCCTACCGAGAAATTTAGGTTCTTAAAGGCTCAGCTGCACAGCAGA	481
482	QY	GCCACATCTATGGGCGCTCACAGGCCACTGTCAGCGGCGAGAGGGGGAGATGCTGGCAC	541
482	Db	GCCACATCTATGGGCGCTCACAGGCCACTGTCAGCGGCGAGAGGGGGAGATGCTGGCAC	541
542	QY	AGCAGCATCGGCTGCGCAGATCCAGGAG-----	570
541	Db	AGCAGCATCGGCTGCGCAGATCCAGGAGAGGTGAGCCTGGCAGCGGTTTGGCAGCAGG	600
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601	Db	GCAGTTGGATGGGGGGCGCACAGGCGAGCTGGAAGGGGGCCCCCTCACCTGGGCTGAGCC	660
571	QY	-----AGATCTCACACGCGGCGGTCTCCAGCCTGAATCTGCCTGGATGAA	616
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617	QY	CTGAGGACCAATCATGCTGCAAGAGAACATCTCCACGCCCCGTGAGGCCCTCTGCAGAGCA	676
721	Db	CTGAGGACCAATCATGCTGCAAGAGAACATCTCCACGCCCCGTGAGGCCCTCTGCAGAGCA	780
677	QY	GGAGTGCTGTTTCACTGGGATCAGCCAGGGCGCGGCCCCCACTTCTGAGCACAAGACA	736
781	Db	GGAGTGCTGTTTCACTGGGATCAGCCAGGGCGCGGCCCCCACTTCTGAGCACAAGACA	840
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961	Db	AAAAAAAAAAAAAAAAAAAAA	984